E3 Cont

enrich for phage to a specific known site. Sequence analysis of these phage would then yield a cluster of peptides which would describe the ligand binding site.--

Please replace the paragraph beginning at page 103, line 2 with the following rewritten paragraph:

--Cellular receptors which span the membrane often need to be in a membrane to take on the correct conformation for a biologically active protein. This presents a problem for conventional techniques designed to find artificial ligands targeted to the native form of the protein. One possible solution to this problem is the use of live cells to express the receptor of choice and then use the whole cell as the way to present the target to the library of artificial ligands. One system in which to do this is the oocyte from Xenopus laevis. We would first clone the receptor of interest into a vector from which RNA could be produced *in vitro* using bacterial or phage RNA polymerases. This RNA would then be injected into oocytes and the oocytes then incubated to allow the production of protein. The oocytes (probably 1-10 per binding reaction), now with the receptor of interest on the cell surface would be mixed with the library of artificial ligands and binding allowed to occur. The oocytes would be washed to remove the non-specific binding ligands and then the ligands would be eluted using a change in pH, salt concentration or another treatment which would break the interaction. The ligands would then be amplified and subjected to further rounds of selection.--

E4

IN THE CLAIMS

Please rewrite claims 22, 25, 26, 27, 30, 34, and 38 as follows:

22 (amended). The panel of claim 27 wherein said peptides

E5

are of the form

$(Xaa)_m$-R1-$(Xaa)_n$,

where R1 is the amino acid at said first fixed position, and m and n do not differ by more than two.

25 (amended). The panel of claim 30 in which the peptides are displayed on chromatographic supports.

26 (amended). The panel of claim 27 in which the peptides are displayed on cells.

27 (amended). A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library having one and only one constant residue at a position fixed for all peptides in all libraries of said panel, wherein, in each library, said fixed position is (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

wherein the amino acid is assigned to said fixed position is not the same in all libraries of said panel,

each library being a separately screenable and physically distinct entity from all other libraries of the panel,

in which the peptides are displayed on viruses.

30 (amended). A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library having one and only one constant residue at a position fixed for all peptides in all libraries of said panel, wherein, in each library, said fixed position is (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

wherein the amino acid is assigned to said fixed position is not the same in all libraries of said panel,

each library being a separately screenable and physically distinct entity from all other libraries of the panel in which the peptides are displayed on viruses